Conclusion

Please consider claims 77-95 when examining the Patent Application. Please debit Deposit Account No. 50-0581 for any requested fees.

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Respectfully submitted,

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:	Affymetrix, Inc. (Michael Mittman)	)
Application No.:	09/396,196	)
Filed:	September 15, 1999	)
		) Art Unit: 1631
For:	METHODS OF GENETIC ANALYSIS USING NUCLEIC ACID ARRAYS	)
Examiner:	Shubo Zhou, Ph.D.	)
Attorney Docket:	04537.0002 / 3101	)

Replacement Claims
Clean Version

77. An array comprising a plurality of nucleic acid probes, wherein said plurality of nucleic acid probes comprises each of the sequences listed in SEQ ID NOS. 1-127,811, or the perfect match or antisense match thereof.

78. The array of claim 77 wherein said array is used to monitor gene expression levels by hybridization to a DNA library.

79. The array of claim 77 wherein said array is used for analysis of genetic variation.

80. The array of claim 77 wherein said array is used for hybridization of tag-labeled compounds.

81. The array of claim 77 wherein said nucleic acid probes are specifically designed for analysis of at least one target sequence.

82. A method of analysis comprising hybridizing one or more nucleic acids to the array of claim 77 and detecting a hybridization pattern.

83. The method of claim 82 wherein said method of analysis comprises monitoring gene expression levels.

84. The method of claim 83 wherein said monitoring gene expression levels comprises comparing gene expression levels of nucleic acids derived from two or more different samples and further comprises the step of:

comparing said hybridization patterns between said nucleic acids derived from said two or more different samples.

85. The method of claim 82 wherein said method of analysis comprises identifying biallelic markers.

86. The method of claim 82 wherein said method of analysis comprises identifying polymorphisms.

87. The method of claim 82 wherein said method of analysis comprises a cross-species comparison wherein the hybridization patterns of a pool of nucleic acids derived from one species are compared with the hybridization patterns of a pool of nucleic acids derived from another species.

88. The method of claim 82 wherein each of said nucleic acids further comprises a tag sequence.

89. The method of claim 82 wherein said method of analysis is a method of identifying family members of a gene.

90. A method comprising using a plurality of probes to probe a sample wherein the plurality of probes comprises each of the sequences listed in SEQ ID NOS. 1-127,811, or the perfect match or antisense match thereof.

91. The method of claim 90 wherein said plurality of probes is used in an *in situ hybridization.*

92. The method of claim 90 wherein said plurality of probes is used to screen cDNA or genomic libraries, or subclones derived from cDNA or genomic libraries, for additional clones containing segments of DNA that have been isolated and previously sequenced.

93. The method of claim 90 wherein said plurality of probes is used in Southern, northern, or dot-blot hybridization to identify or detect the sequence of any gene.

94. The method of claim 90 wherein said plurality of probes is used in Southern or dot-blot hybridization of genomic DNA to detect specific mutations in any gene.

95. The method of claim 90 wherein said plurality of probes is used to map the 5' termini of mRNA molecules by primer extensions.